STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/700,816A_

Source: _____

Date Processed by STIC: _7/14/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual** - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

SERIAL NUMBER: _10/700, 816A_

ERROR DETECTED	SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11 _____ Use of <220> — Sequence(s) /6 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12 _____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

IFW16

RAW SEQUENCE LISTING   DATE: 07/14/2006
PATENT APPLICATION: US/10/700,816A   TIME: 09:11:02

Input Set : A:\new SEQLIST txt.txt
Output Set: N:\CRF4\07142006\J700816A.raw

```
 4 <110> APPLICANT: Xu, Zuoshang and Zamore, Phillip D.
 6 <120> TITLE OF INVENTION: Allele-Specific RNA Interference
 9 <130> FILE REFERENCE: UMY-038
11 <140> CURRENT APPLICATION NUMBER: 10/700816A
12 <141> CURRENT FILING DATE: 2003-11-04
14 <150> PRIOR APPLICATION NUMBER: 60/423,507
15 <151> PRIOR FILING DATE: 2002-11-04
17 <150> PRIOR APPLICATION NUMBER: 60/488,283
18 <151> PRIOR FILING DATE: 2003-07-18
20 <160> NUMBER OF SEQ ID NOS: 19
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

see pr 2-3, 5

*Does Not Comply
Corrected Diskette Needed*

ERRORED SEQUENCES

P.2

```
280 <210> SEQ ID NO: 19
281 <211> LENGTH: 2288
282 <212> TYPE: DNA
283 <213> ORGANISM: Homo sapiens
285 <400> SEQUENCE: 19
286 gtaccctgtt tacatcattt tgccattttc gcgtactgca accggcgggc cacgccgtga 60
287 aaagaaggtt gttttctcca cagtttcggg gttctggacg tttcccggct gcggggcggg 120
288 gggagtctcc ggcgcacgcg gccccttggc ccgcccagt cattccggc cactcgcgac 180
289 ccgaggctgc cgcaggggc gggctgagcg cgtgcgaggc cattggtttg gggccagagt 240
290 gggcgaggcg cggaggtctg gcctataaag tagtcgcgga gacggggtgc tggtttgcgt 300
291 cgtagtctcc tgcaggtctg gggtttccgt tgcagtcctc ggaaccagga cctcggcgtg 360
292 gcctagcgag ttatggcgac gaaggccgtg tgcgtgctga agggcgacgg cccagtgcag 420
293 ggcatcatca atttcgagca gaaggcaagg gctgggaccg ggaggcttgt gttgcgaggc 480
294 cgctcccgac ccgctcgtcc ccccgcgacc ctttgcatgg acgggtcgcc cgccagggct 540
295 agagcagtta agcagcttgc tggaggttca ctggctagaa agtggtcagc ctgggattgc 600
296 atggacggat ttttccactc ccaagtctgg ctgcttttta cttcactgtg aggggtaaag 660
297 gtaaatcagc tgttttcttt gttcagaaac tctctccaac tttgcacttt tcttaaagga 720
298 aagtaatgga ccagtgaagg tgtgggggaag cattaaagga ctgactgaag gcctgcatgg 780
299 attccatgtt catgagtttg gagataatac agcaggtggg tcataattta gcttttttttt 840
300 cttcttctta taaataggct gtaccagtgc aggtcctcac tttaatcctc tatccagaaa 900
301 acacggtggg ccaaaggatg aagagaggta acaagatgct taactcttgt aatcaatggc 960
302 gatacgtttc tggagttcat atggtatact acttgtaaat atgtgcctaa gataattccg 1020
303 tgtttccccc acctttgctt ttgaacttgc tgactcatgt gaaaccctgc tcccaaatgc 1080
304 tggaatgctt ttacttcctg ggcttaaagg aattgacaaa tgggcactta aaacgatttg 1140
305 gttttgtagc atttgattga atatagaact aatacaagtg ccaaaggga actaatacag 1200
306 gaaatgttca tgaacagtac tgtcaaccac tagcaaaatc aatcatcatt tgatgctttt 1260
307 catataggca tgttggagac ttgggcaatg tgactgctga caaagatggt gtggccgatg 1320
308 tgtctattga agattctgtg atctcactct caggagacca ttgcatcatt ggccgcacac 1380
```

RAW SEQUENCE LISTING   DATE: 07/14/2006
PATENT APPLICATION: US/10/700,816A   TIME: 09:11:02

Input Set : A:\new SEQLIST txt.txt
Output Set : N:\CRF4\07142006\J700816A.raw

```
309 tggtggtaag ttttcataaa ggatatgcat aaaacttctt ctaacagtac agtcatgtat 1440
310 ctttcacttt gattgttagt cgcgaattct aagatccaga taaactgtgt ttctgctttt 1500
311 aaactactaa atattagtat atctctctac taggattaat gttattttc taatattatg 1560
312 aggttcttaa acatctttg ggtattgttg ggaggaggta gtgattactt gacagcccaa 1620
313 agttatcttc ttaaaatttt ttacaggtcc atgaaaaagc agatgacttg ggcaaaggtg 1680
314 gaaatgaaga aagtacaaag acaggaaacg ctggaagtcg tttggcttgt ggtgtaattg 1740
315 ggatcgccca ataaacattc ccttggatgt agtctgaggc cccttaactc atctgttatc 1800
316 ctgctagctg tagaaatgta tcctgataaa cattaaacac tgtaatctta aaagtgtaat 1860
317 tgtgtgactt tttcagagtt gctttaaagt acctgtagtg agaaactgat ttatgatcac 1920
318 ttggaagatt tgtatagttt tataaaactc agttaaaatg tctgtttcaa tgacctgtat 1980
319 tttgccagac ttaaatcaca gatgggtatt aaacttgtca gaatttcttt gtcattcaag 2040
320 cctgtgaata aaaaccctgt atggcactta ttatgaggct attaaaagaa tccaaattca 2100
321 aactaaatta gctctgatac ttatttatat aaacagcttc agtggaacag atttagtaat 2160
322 actaacagtg atagcatttt attttgaaag tgtttgaga ccatcaaaat gcatacttta 2220
323 aaacagcagg tctttagct aaaactaaca caactctgct tagacaaata ggctgtcctt 2280
324 tgaagctt                                                         2288
```

E--> 325 umy-038   delete
E--> 330 1

```
<210> 1
<211> 21
<212> RNA
<213> Artificial Sequence

<220>
<223> synthetic

<221> misc_feature
<222> 20, 21
<223> n=deoxy thymidine

<400> 1
uggagacuug cgcaaugugn n
```

t's not allowed in an RNA sequence, even if they're represented

21 *by n's*

for a combined DNA/RNA sequence, use <2127 DNA and explain in <2207-<2237 section

same error in seqs. 2-6, 9-14

VERIFICATION SUMMARY   DATE: 07/14/2006
PATENT APPLICATION: US/10/700,816A   TIME: 09:11:03

Input Set : A:\new SEQLIST txt.txt
Output Set: N:\CRF4\07142006\J700816A.raw

L:32 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:36 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:47 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:51 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:62 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:67 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:78 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:82 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:83 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:93 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:97 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:98 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:108 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:112 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:139 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:143 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:154 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:158 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:169 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:173 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:184 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:188 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:199 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:203 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:214 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:218 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:234 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:16, <213>
ORGANISM:Artificial Sequence
L:234 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:16, <213>
ORGANISM:Artificial Sequence
L:234 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:234
L:325 M:254 E: No. of Bases conflict, LENGTH:Input:-38 Counted:2292 SEQ:19
L:325 M:112 C: (48) String data converted to lower case,
M:254 Repeated in SeqNo=19
L:330 M:252 E: No. of Seq. differs, <211> LENGTH:Input:2288 Found:2292 SEQ:19

```
<210> 16
<211> 52
<212> RNA
<213> Artificial Sequence    see item 11 on Error Summary Sheet

<400> 16
gacaaagaug cuguggccga uaagcuuauc ggccacagca ucuuugucuu uu          52
```